

## **Amendments to the Claims**

1. **(Currently Amended)** A nucleic acid array comprising:  
a solid support; and  
a plurality of nucleic acid probes attached to the solid support at discrete locations,  
wherein at least one of the probes is an alien probe in that it has a sequence that is alien to a  
hybridizing mixture to be hybridized to the array;  
and further wherein the sequence of the alien probe comprises a sequence that is  
generated by applying a Hidden Markov Model algorithm to the natural sequence statistics of  
one or more naturally-occurring sequences of interest to generate a model sequence,  
with the proviso that, at an adjustable frequency, a sequence statistic of the one or more  
naturally-occurring sequences of interest is switched to a sequence statistic that is inversely  
proportional to the natural sequence statistic,  
such that the alien sequence comprises intermittent highly improbable sequence patterns  
or subsequences throughout its length,  
wherein the alien probe comprises a sequence selected from the group consisting of SEQ  
ID NOs: 1-150.  
~~and with the further proviso that the alien sequence does not occur naturally in any~~  
~~organism.~~
2. **(Original)** The nucleic acid array of claim 1, wherein the hybridizing mixture comprises  
nucleic acids from a source selected from the group consisting of human mRNA, human cDNA,  
mouse cDNA, mouse mRNA, and combinations thereof.
3. **(Original)** The nucleic acid array of claim 1, wherein the alien probe is present in each  
discrete location on the solid support.
- 4-13. **(Canceled)**
14. **(Previously Presented)** The nucleic acid array of claim 1, wherein the adjustable  
frequency comprises a frequency between about 1 in 5.
15. **(Previously Presented)** The nucleic acid array of claim 1, wherein the adjustable  
frequency comprises a frequency between about 1 in 10.

**16. (Previously Presented)** The nucleic acid array of claim 1, wherein the sequence statistic that is switched is selected from the group consisting of: codon occurrence, codon boundary di-nucleotide frequencies, and combinations thereof.

**17-18. (Canceled)**